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1 10 20 30
 NEP1-HU MGK.....SESQMDITDINT..PKPKKKQRWTPLEI.....SLSVLVLLL
 * * * * *
 PEX-HUM MEA.....ETG....SSVET..GKKANRGTRIALVV.....FVGGTLVLG
 ** * * * * *
 KELL-HU MEGGDQSEEEPRERSQAGGMGTLSQESTPEERLPVEGSRPWAV....ARRVLTAILIL.
 * * * * *
 ECE1-HU MSTYKRATLDEEDLVDSLSEGDAYPNGLQVNFHSPRSGQRCWAARTQVEKRLVVLVVLLA
 * * * * *
 consens M T P L

40 50 60 70 80 90
 NEP1-HU TIIAVTMIALYA.TYDD...GICKSSDCIKSAARLIQNMDATTEPCTDFFKYACGGWLKR
 ** * * * * *
 PEX-HUM TILFLVSQGLLSLQAKQ...EYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGIWISN
 * * * * *
 KELL-HU .GLLLCFSVLLFYNFQNCGPRPCETSVCLDLDRDHYLASGNTSVAPCTDFFSFACG...RA
 ** * * * * *
 ECE1-HU AGLVACLALGI.QYQTRSPSVCLSEACVSVTSSILSSMDPTVDPCHDFFSYACGGWIK
 * * * * *
 consens L L C C L V PC DFF ACGGW

100 110 120 130 140 150
 NEP1-HU NVIPETSSRYGNFDILRDELEVVLKDVLPQEP..KTEDIVAVQKAKALYRSCINESAIDSR
 * * * * *
 PEX-HUM NPIPEDMPSYGVYPWLRHNVLDLKLKELLEKSISRDRDETAIQKAKILYSSCMNEKAIEKA
 * * * * *
 KELL-HU KETNNS.....FQELATKNKNRRLRILEVQ.NSWHPGSGEKAQFQYNSCMDTLAIEAA
 * * * * *
 ECE1-HU NPVPDGHRSRWTFSNLWEHNQAIKHLLENS.TA.SVSEAERKAQVYRACMNETRIEEL
 * * * * *
 consens N P G F L LK LE A KA Y SCMNE AIE

160 170 180 190 200
 NEP1-HU GGEPLKLLPDI.YGWP..VATENWEQKYGAS.WTAEKAIQNLNSKYGKKVLINLFGVTD
 ** * * * * *
 PEX-HUM DAKPLHLRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGOYSNSVFIRLYVSPD
 ** * * * * *
 KELL-HU GTGPLRQVIEEL.....GGWRISGKWTSLNFN..RTLRLMSQYGHFFFRAYLGP
 ** * * * * *
 ECE1-HU RAKPLMELIERL.....GGWNITGPWAKDNFQ..DTLQVVTAHYRTSPFFSVVVSAD
 * * * * *
 consens PL G W F TL Y F YV D

220 230 240 250 260
 NEP1-HU DKNSVNHVIHIDQPRGLPSR.DYECTGIYKEACTAYVDFMISVARLIRQEERLPI.DE
 ** * * * * *
 PEX-HUM DKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVL.....LGA.NS
 ** * * * * *
 KELL-HU PASPHTPVIQIDQPEFDVPLKQDQEQKI.YAQIFRE.YLTYLNQLGTL.....LGG.DP
 ** * * * * *
 ECE1-HU SKNSNSNVIQVDQSGGLPSRDYLLNKTENEKVLTG.YLNYMVQLGKL.....LGGGDE
 * * * * *
 consens K S VI DQ L LP R DY K Y M L LG D

FOR "SECRET"

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	560	570	580	590	600	610
NEP1-HU	AGILQPPFFSAQQ.SNSLNYGGIGMVGHEITHGFDDNGRNFNKDGDLDVDWWTQQSASNF					
	** ** *	** ** *	** ** *	** ** *	** ** *	** ** *
PEX-HUM	AGELQKPPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDDNNGRKYDKNGNLDPWWSTESEEFK					
	** ** *	** ** *	** ** *	** ** *	** ** *	** ** *
KELL-HU	AGLLQPPFFHPGY.PRAVNFGAAGSIMAHELLHIFYQL...LLPGGCL...ACDNHAL					
	** ** *	** ** *	** ** *	** ** *	** ** *	** ** *
ECE1-HU	AGILQAPFYTRSS.PKALNFGGIGVVVGHETHAFDDQGREYDKDGNLRPWWKNSSVEAF					
consens	AG LQ PFF	P L N G I G	G H E T H F D	G R	K G L W W	S F

	620	630	640	650	660	670
NEP1-HU	KEQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGLGQAYRAYQNYI..KKNNG.EE					
	** ** *	** ** *	** ** *	** ** *	** ** *	** ** *
PEX-HUM	KEKTKCMINQYSNYYWK.KAGLNVK GKRTLGENIADNGGLREAFRAYRKWINDRRQGLEE					
	** ** *	** ** *	** ** *	** ** *	** ** *	** ** *
KELL-HU	QEAHLCLKRHYAAF..PLPSRTSFNDSLTFLENAADVGGLAIALQAYS KRL..LRHH.GE					
	** ** *	** ** *	** ** *	** ** *	** ** *	** ** *
ECE1-HU	KRQTECMVEQYSNY..SVNG.EPVNGRHTLGENIADNGGLKAAYRAYQNWV..KKNNG.AE					
consens	KE CM QY N		NG T L G E N I A D N G G L	(3)	A R A Y	G E

	680	690	700	710	720	730
NEP1-HU	KLLPGLDLN HKQLFFLNFAQVWC TYRPEYAVNSIKTDVHSPGNFRIIGTLQNSAEFSEA					
	** ** *	** ** *	** ** *	** ** *	** ** *	** ** *
PEX-HUM	PLLPGITFTNNQLFFLSYAHVRC HSYRPEAAREQVQIGAHSPQFRVNGAISNFEEFQKA					
	** ** *	** ** *	** ** *	** ** *	** ** *	** ** *
KELL-HU	TVLPSLDLSPQQIFFRSYAQVMCRKPSQD SH...DTHSPPHLRVHGPLSSTPAFARY					
	** ** *	** ** *	** ** *	** ** *	** ** *	** ** *
ECE1-HU	HSLPTLGLTNNQLFFLGFAQVWC SVRTPESSHEGLITDPHSPSRFRVIGSLSNSKEFSEH					
consens	LP L L	QLFFL	AQV C	PE	D H S P	FRV G L S N E F

	740	750
NEP1-HU	FHCRKNSYMNPEKK.CR VW	
	** ** *	** ** *
PEX-HUM	FNCPPNSTMNRGMDSCRLW	
	** ** *	** ** *
KELL-HU	FRCARGALLNPSSR.CQLW	
	** ** *	** ** *
ECE1-HU	FRCPPGSPMPPHK.CEVW	
consens	F C S M N P	C W

FORBIO" 6222660

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PRIMER	SEQUENCE
(1A)	5'-TGGATGGAT/CGA/CIGG/AIACIA/CA-3'
(1B)	5'-TGGATGGAT/CGA/CIGG/AIACIA/CG-3'
(2A)	5'-A/GTIGTTTT/CCCIGCIGGIA/GT/AIC/TTA/TCA-3'
(2B)	5'-A/GTIGTTTT/CCCIGCIGGIA/GT/AIC/TTG/CCA-3'
(3)	5'-AIIICCICCA/TC/TA/GTCIGCIG/AC/TA/GTTT/CTC-3'
(4)	5'-GAT/CAAT/CT/CTIGAT/CGAA/GT/CTIAAT/CTGGATGG-3'
(5)	5'-T/CT/CACCAIATICT/GA/GCATCG/TT/CTTCATIGGG/ATG-3'

FIGURE 6

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ala thr met leu arg lys asp gln asn leu ser lys glu ser ala met val arg glu glu met ala glu val leu glu leu glu thr his
811 GCC ACT ATG CTT AGG AAA GAC CAG AAC CTG TCC AAG GAG AGC GCC ATG GTG CGG GAG GAG ATG CCG GAG GTG CTG GAA CTG GAG ACG CAT
leu ala asn ala thr val pro gln glu lys arg his asp val thr ala leu tyr his arg met asp leu met glu leu gln glu arg phe
901 CTG GCC AAC GCC ACA GTC CCC CAG GAG AAA AGG CAT GAT GTC ACT GCC CTG TAC CAC CGA ATG GAC CTG ATG GAG CTA CAG GAA AGG TTT
gly leu lys gly phe asn trp thr leu phe ile gln asn val leu ser ser val glu val glu leu phe pro asp glu glu val val
991 GGT CTG AAG GGG TTT AAC TGG ACT CTC TTC ATA CAA AAC GTG TGG TCT TCT GTG GAA GTC GAG CTG TTC CCA GAT GAG GTG GTG GTC
tyr gly ile pro tyr leu glu asn leu glu asp ile ile asp ser tyr ser ala arg thr met gln asn tyr leu val trp arg leu val
1081 TAC GCC ATC CCC TAC CTG GAG AAT CTG GAG GAT ATC ATT GAT ACC TAC TCA GCA CGG ACC ATG CAG AAC TAC CTG GTA TGG CGC CTG GTG
leu asp arg ile gly ser leu ser gln arg phe lys glu ala arg val asp tyr arg lys ala leu tyr gly thr thr val glu glu val
1171 CTA GAT CGA ATT GGC AGC CTG AGC CAG AGA TTC AAA GAG GCG CGT GTG GAC TAC CGC AAG GCG CTG TAC GGC AGG ACC GTG GAG GTA
arg trp arg glu cys val ser tyr val asn ser asn met glu ser ala val gly ser leu tyr ile lys arg ala phe ser lys asp ser
1261 CGC TGG CGA GAG TGT GTC ACC TAT GTC AAC AGT AAC ATG GAG AGC GCC GTG GGC TCC CTC TAC ATC AAG CCG GCC TTC TCC AAG GAC AGC
lys ser thr val arg glu leu ile glu lys ile arg ser val phe val asp asn leu asp glu leu asn trp met asp glu glu ser lys
1351 AAG AGC ACG GTC AGA GAG CTG ATT GAG AAG ATA AGG TCC GTG TTT GTG GAT AAC CTG GAG CTG AAC TGG ATG GAC GAG GRA TCC AAG
lys lys ala gln glu lys ala met asn ile arg glu gln ile gly tyr pro asp tyr ile leu glu asp asn asn lys his leu asp glu
1441 AAG AAG GCC CAG GRA AAG GCC ATG AAT ATA CCG GAA CAG ATT GGC TAC CCT GAC TAC ATT TTG GAA GAT AAC AAT AAA CAC CTG GAT GAG
glu tyr ser ser leu thr phe tyr glu asp leu tyr phe glu asn gly leu gln asn leu lys asn ala gln arg ser leu lys lys
1531 GAA TAC TCC AGT TTG ACT TTC TAT GAG GAC CTC TAT TTT GAG AAC GGA CTT CAG AAC CTC AAG AAC AAT GCC CAG AGG AGC CTC AAG AAG
leu arg glu lys val asp gln asn leu trp ile ile gly ala ala val val asn ala phe tyr ser pro asn arg asn gln
1621 CTT CGG GAA AAG GTG GAC CAG AAT CTC TGG ATC ATC GGG GCT GCA GTG GTC AAT GCA TTC TAC TCC CCA AAC AGA AAC CAG ATC GTC TTT

~~SECRET~~ (cont'd)

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1711 pro ala gly ile leu gln pro pro phe phe ser lys asp gln pro gln ser leu ser leu asn phe gly gly ile gly met val ile gly his glu
 CCA GCA GGG ATT CTC CAG CCG CCC TTC TTC AGC AAG GAC CAA CCA CAG TCC TTG AAT TTT GGG GGC ATC GGG ATG GTG ATT GGG CAC GAG
 1801 ile thr his gly phe asp asp asp gly arg asn phe asp lys asn met leu asp trp trp ser asn phe ser ala arg his phe
 ATC ACA CAC GGC TTT GAT GAT AAT GGT CGT AAC TTT GAC AAG AAC GGC AAC ATG CTG GAC TGG TGG AGT AAC TTC TCG GCC CGG CAC TTC
 1891 gln gln gln ser gln cys met ile tyr gln tyr gly asn phe ser trp glu leu ala asp asn gln asn val asn gly phe ser thr leu
 CAA CAG CAG TCG CAA TGC ATG ATC TAT CAG TAC GGC AAC TTC TCT TGG GAA CTA GCA GAC AAC CAG AAT GTG AAC GGA TTC AGT ACC CTC
 1981 gly glu asn ile ala asp asn gly gly val arg gln ala tyr lys ala tyr leu arg trp leu ala asp gly gly lys asp gln arg leu
 GGG GAG AAC ATT GCC GAC AAC GGA GGT GTG CGA CAG GCA TAC AAG GCT TAC CTA CGG TGG CTG GCT GAT GGC GGC AAA GAT CAG CGA CTG
 2071 pro gly leu asn leu thr tyr ala gln leu phe phe ile asn tyr ala gln val trp cys gly ser tyr arg pro glu phe ala val gln
 CCG GGA CTG AAC CTG ACC TAT GCC CAG CTT TTC TTC ATC AAC TAT GCC CAG GTG TGG TGT GGG TCC TAT AGG CCG GAG TTC GCC GTC CAG
 2161 ser ile lys thr asp val his ser pro leu lys tyr arg val leu gly ser leu gln asn leu pro gly phe ser glu ala phe his cys
 TCC ATC AAG ACG GAC GTC CAC AGT CCT CTT AAG TAC AGG GTG CTG GGC TCA CTA CAG AAC CTG CCA GGC TTC TCT GAG GCA TTC CAC TGC
 2251 pro arg gly ser pro met his pro met lys arg cys arg ile trp ***
 CCA CGA GGC AGC CCC ATG CAC CCC ATG AAG CGA TGT CGC ATC TGG TAG CCAAGGCTGAGTATGCTGGGCCACCGCCCGCCACCCAGAGGGCTTCGGCAATG
 2354 GTGTAGCTGGCAGAGATGTCCAGGTCTTTGCCCTGAAGGCCACCGGAGCCACCCAGCCCGCCCTCCCGCCAGCTAGAGTGTAGCCACCCCGCCACCCCGGGATGAGTGGTGCCGGTC
 2473 CTGCGCCCTCAGGCCAGTGAGGGTTCAGCAGCCCGAGGAGAGCAGTCAAGTGCCTTCCACCCCTCTCCATAGTGTGTGGCTAAATGTTCTCGAGCTTCAGACTTGAGCTAAGTAAACGC
 2925 TTC

FIG. 3 (cont'd)

901 val leu glu leu glu thr gln thr gln thr gln thr val pro gln glu glu arg his asp val ile ala leu tyr his arg met gly leu
 GTT CTG GAG CTG GAG ACA CAG CAG CTG GCC AAG GCC ACG GTA CCC CAG GAG GAG AGA CAC GAC GAC GTC ATC GCC TTG TAC CAC CCG ATG GGA CTG
 358
 991 glu glu leu gln ser gln phe phe gly leu lys gly phe asn trp thr leu phe ile gln thr thr val lys ile lys leu leu
 GAG GAG CTG CAA AGC CAG TTT GGC CTG AAG GGA TTT AAC TGG ACT CTG TTC ATA CAA ACT GTG CTA TCC TCT GTC AAA ATC AAG CTG CTG
 388
 1081 pro asp glu glu val val tyr gly ile pro tyr leu gln asn leu glu asn ile ile asp thr tyr ser ala arg thr ile gln asn
 CCA GAT GAG GAA GTG GTG GTC TAT GGC ATC CCC TAC CTG CAG AAC CTT GRA AAC ATC ATC GAC ACC TAC TCA GCC AGG ACC ATA CAG AAC
 418
 1171 tyr leu val trp arg leu val leu asp arg ile gly ser leu ser gln arg phe lys asp thr arg val asn tyr arg lys ala leu phe
 TAC CTG GTC TGG CCG CTG GTG CTG GAC CGC ATT GGT AGC CTA AGC CAG AGA TTC AAG GAC ACA CGA GTG AAC TAC CGC AAG GCG CTG TTT
 448
 1261 gly thr met val glu glu val arg trp arg glu cys val gly tyr val asn ser asn met glu asn ala val gly ser leu tyr val arg
 GGC ACA ATG GTG GAG GAG GTG CCG TGG CGT GAA TGT GTG GGC TAC GTC AAC AGC AAC ATG GAG AAC GCC GTG GGC TCC CTC TAC GTC AGG
 478
 1351 glu ala phe pro gly asp ser lys ser met val arg glu leu ile asp lys val arg thr val phe val glu thr leu asp glu leu gly
 GAG GCG TTC CCT GGA GAC AGC RAG AGC ATG GTC ACA GAA CTC ATT GAC AAG GTG CCG ACA GTG TTT GTG GAG ACG CTG CAC GAG CTG GGC
 508
 1441 trp met asp glu glu ser lys lys lys ala gln glu lys ala met ser ile arg glu gln ile gly his pro asp tyr ile leu glu glu
 TGG ATG GAC GAG GAG TCC AAG AAG AAG GCG CAG GAG AAG GCC ATG AGC ATC CCG GAG CAG ATC GGG CAC CCT GAC TAC ATC CTG GAG
 538
 1531 met asn arg arg leu asp glu tyr ser asn leu asn phe ser glu asp leu tyr phe glu asn ser leu gln asn leu lys val gly
 ATG AAC AGG CCG CTG GAC GAG GAG TAC TCC AAT CTG AAC TTC TCA GAG GAC CTG TAC TTT GAG AAC AGT CTG CAG AAC CTC AAG GTG GGC
 568
 1621 ala gln arg ser leu arg lys leu arg glu lys val asp pro asn leu trp ile ile gly ala ala val val asn ala phe tyr ser pro
 GCC CAG CCG ACC CTC AGG AAG CTT CCG GAA AAG GTG GAC CCA AAT CTC TGG ATC ATC GGG CCG GCG GTG GTC AAT GCG TTC TAC TCC CCA
 598
 1711 asn arg asn gln ile val phe pro ala gly ile leu gln pro phe phe ser lys glu gln pro gln ala leu asn phe gly gly ile
 AAC CGA AAC CAG ATT GTA TTC CCT GCC GGG ATC CTC CAG CCC TTC TTC AGC AAG GAG CAG CCA CAG GCC TTG AAC TTT GGA GGC ATT
 628

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FIG - 4 (cont'd)

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gly met val ile gly his glu ile thr his gly phe asp asp asn gly arg arg asn phe asp lys asn gly asn met met asp trp trp ser
1801 GGG ATG GTG ATC GGG CAC GAG ATC ACG CAC GGC TTT GAC GAC AAT GGC AAT GGC AAC ATG ATG ATG GAT TGG TGG AGT 658

asn phe ser thr gln his phe arg glu gln ser glu cys met ile tyr gln tyr gly asn tyr ser trp asp leu ala asp glu gln asn
1891 AAC TTC TCC ACC CAG CAC TTC CGG GAG CAG TCA GAG TGC ATG ATC TAC CAG TAC GGC AAC TAC TCC TGG GAC CTG GCA GAC GAA CAG AAC 658

val asn gly phe asn thr leu gly glu asn ile ala asp asn gly glu val arg gln ala tyr lys ala tyr leu lys trp met ala glu
1981 GTG AAC GGA TTC AAC ACC CTT GGG GAA AAC AAT GCT GAC AAC GGA GGG GTG CCG CAA GCC TAT AAG GCC TAC CTC AAG TGG ATG GCA GAG 688

gly gly lys asp gln gln leu pro gly leu asp thr his glu gln leu phe phe ile asn tyr ala gln val trp cys gly ser tyr
2071 GGT GGC AAG GAC CAG CAG CTG CCC GGC CTG GAT CTC ACC CAT GAG CAG CTC TTC TTC ATC AAC TAT GCC CAG GTG TGG TGC GGG TCC TAC 718

arg pro glu phe ala ile gln ser ile lys thr asp val his ser pro leu lys tyr arg val leu gly ser leu gln asn leu ala ala
2161 CGG CCC GAG TTC GCC ATC CAA TCC ATC AAG ACA GAC GTC CAC ACT CCC CTG AAG TAC AGG GTA CTG GGG TCG CTG CAG AAC CTG GCC GCC 748

phe ala asp thr phe his cys ala arg gly thr pro met his pro lys glu arg cys arg val trp ter
2251 TTC GCA GAC ACG TTC CAC TGT GCC CGG GGC ACC CCC ATG CAC CCC AAG GAG CGA TGC CGC GTG TGG TAG CCA AGG CCC TGC CGC GCT GTG 770

2341 CGG CCC ACG CCC ACC CGC TGC TCG GAG GCA TCT GTG CGA AGG TGC AGC TAG CGG CGA CCC AGT GTA CGT CCC GCC CCG GCC AAC CAT GCC 688

2431 ARG CCT GCC TGC CAG GCC TCT GCG CCT GGC CTA GGG TGC AGC CAC CTG CCT GAC ACC CAG GGA TGA GCA GTG TCC AGT GCA GTA CCT GGA 688

2521 CCG GAG CCC CCT TCA CAG ACA CCC GCG GGC CTC AGT GCC CCC GTC ACA ACT CTG TAG AGA GAA TCA ACT GTG TCC TGC CCA CCC TTC AAG 688

2611 GTG CAT TGT CTT CCA GTA TCT ACA GCT TCA GAA CTT GAG CTA AGT AAA TGC TTT CAA AGA AAA AAA

FFS - 4 (cont'd)

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1171 ile thr val ser glu tyr asp asp leu arg arg asp val ser ser met tyr asn lys val thr leu gly gln leu gln lys ile thr pro
 ATC ACT GTG TCA GAG TAT GAC GAC CTA CGG CGA GAT GTC AGC TCC ATG TAC AAC AAG GTG ACC CTG GGG CAG CTG CAG AAG ATC ACC
 382
 1261 his leu arg trp lys trp leu leu asp gln ile phe gln glu asp phe ser glu glu glu val val leu leu ala thr asp tyr met
 CAC TTG CGG TGG AAG TGG CTG CTA GAC CAG ATC TTC CAG GAG GAC TTC TCA GAG GAA GAG GTG GTG CTG CAG GCG ACA GAC TAC ATG
 412
 1351 gln gln val ser gln leu ile arg ser thr pro his arg val leu his asn tyr leu val trp arg val val leu ser glu his
 CAG CAG GTG TCG CAG CTC ATC CGC TCC ACA CCC CAC CGG GTC CTG CAC AAC TAC CTG GTG TGG CGC GTG GTG GTC CTG AGT GAA CAC
 442
 1441 leu ser pro pro phe arg glu ala leu his glu leu ala gln glu met glu gly ser asp lys pro gln glu leu ala arg val cys leu
 CTG TCC CCG CCA TTC CGT GAG GCA CTG CAG GAG CTG GCA CAG GAG ATG GAG GGC AGC GAC AAG CCA CAG GAG CTG GCC CGG GTC TGC TTG
 472
 1531 gly gln ala ala asn arg his phe gly met ala leu gly ala leu phe val his glu his phe ser ala ala ser lys ala lys val gln gln
 GGC CAG GCC AAT CGC CAC TTT GGC ATG GCG CTT GGC GCC CTC TTT GTA CAT GAG CAC TTC TCA GCT GCC AGC AAA GCC AAG GTG CAG CAG
 502
 1621 leu val glu asp ile lys tyr ile leu gly gln arg leu glu leu asp trp met asp ala glu thr arg ala ala arg ala
 CTA GTG GAA GAC ATC AAG TAC ATC CTG GGC CAG CGC CTG GAG GAG CTG GAC TGG ATG GAC GCC GAG ACC AGG GCT GCT CGG GCC AAG
 532
 1711 leu gln tyr met met val met val gly tyr pro asp phe leu leu lys pro asp ala val asp lys glu phe glu val his glu
 CTC CAG TAC ATG ATG GTG ATG GTC GGC TAC CCG GAC TTC CTG CTG AAA CCC GAT GCT GTG GAC AAG GAG TAT GAG TTT GAG GTC CAT GAG
 562
 1801 lys thr tyr phe lys asn ile leu asn ser ile arg phe ser ile gln leu ser val lys lys ile arg gln glu val asp lys ser thr
 AAG ACC TAC TTC AAG AAC ATC TTG AAC AGC ATC CCC TTC AGC ATC CAG CTC TCA GTT AAG AAG ATT CGG CAG GAG GTG GAC AAG TCC ACC
 592
 1891 trp leu leu pro pro gln ala leu asn ala leu pro asn lys asn gln met val phe pro ala gly ile leu gln pro thr leu
 TGG CTG CTC CCC CCA CAG GCG CTC AAT GCC TAC TAT CTA CCC AAC AAG AAC CAG ATG GTG TTC CCC GCG GGC ATC CTG CAG CCC ACC CTG
 622
 1981 tyr asp pro asp phe pro gln ser leu asn tyr gly gly ile gly thr ile ile gly his glu leu thr his gly tyr asp asp trp gly
 TAC GAC CCT GAC TTC CCA CAG TCT CTC AAC TAC GGG GGC ATC GGC ACC ATC ATT GGA CAT GAG CTG ACC CAC GGC TAC GAC TGG GGG
 652

FRS - 5 (cont'd)

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gly gln tyr asp arg ser gly asn leu leu leu his trp trp thr glu ala ser tyr ser arg phe leu arg lys ala glu cys ile val arg
2071 GGC CAG TAT GAC GAC CGC TCA GGC AAC CTG CTG CAC TGG TGG ACG GAG GCC TCC TAC AGC CGC TTC CTG CGA AAG GCT GAG TGC ATC GTC CGT 682

leu tyr asp asn phe thr val tyr asn gln arg arg glu val asn gly lys his thr leu gly glu asn ile ala asp met gly gly leu lys leu
2161 CTC TAT GAC AAC TTC ACT GTC TAC AAC CAG CGG GIG AAC GGG AAA CAC ACG CTT GGG GAG AAC ATC GCA GAT ATG GGC GGC CTC AAG CTG 712

ala tyr his ala tyr gln lys trp val arg glu his gly pro glu his pro leu pro arg leu lys tyr thr his asp gln leu phe phe
2251 GCC TAC CAC GCC TAT CAG AAG TGG GTG CGG GAG CAC GGC CCA GAG CAC CCA CTT CCC CGG CTC AAG TAC ACA CAT GAC CAG CTC TTC TTC 742

ile ala phe ala gln asn trp cys ile lys arg arg ser gln ser ile tyr leu gln val leu thr asp lys his ala pro glu his tyr
2341 ATT GCC TTT GCC CAG AAC TGG TGC ATC AAG CGG CGG TCG CAG TCC ATC TAC CTG CAG GTG CTG ACT GAC AAG CAT GCC CCT GAG CAC TAC 772

arg val leu gly ser val ser gln phe glu glu phe gly arg val leu his cys pro lys val ser pro met asn pro ala his lys cys
2431 AGG GTG CTG GGC AGT GTG TCC CAG TTT GAG GAG TTT GGC CGG GTT TTA CAC TGT CCA AAG GTC TCA CCC ATG AAC CCT GCC CAC AAG TGT 775

ser val trp ter

2521 TCC GTG TGG TGA CCC TGG CTG CCC GCC TGC ACG CCC CCA CTG CCC CCG CAC GAA TCA CCT CCT GCT GGC TAC CGG GGC AGG CAT GCA CCC

2611 GGT GCC AGC CCC GCT CTG GGC ACC ACC TGC CTT CCA GCC CCT CCA GGA CCC GGT CCC CCT GGT GCC CCT CAC TTC AAG AGG GGC CTG GAG

2701 CAG GGT GAG GCT GGA CTT TGG GGG GCT GTG AAG GAA ATA TAC TGG GGT CCC CAG ATT CTG CTC TAA GGG GGC CAG ACC CTC TGC CAG GCT

2791 GGA TTG TAC GGG CCC CAC CTT CGC TGT GTT GCT GCA AGT CTG GTC AAA TAA ATC ACT GCA CTG TTA AAA AAA AAA AAA

~~SECRET~~ - 5 (cont'd)

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560 570 580 590 600 610
 NEP-HUM VFPAGILQPPFFSAQQSNLSLNYGGIGMVGHEITHGFDDNGRNFNKDGDLDVDWWTQQSAS
 ***** * * * * * * * * *
 NL1-MOU VFPAGILQPPFFSKDQPQSLNFGGIGMVGHEITHGFDDNGRNFDKNGNMLDWWSNFSAR
 ***** * * * * * * * * *
 NL2-HUM VFPAGILQPPFFSKEQPQALNFGGIGMVGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQ
 ***** * * * * * * * * *
 NL3-HUM VFPAGILQPTLYDPDFPQSLNYGGIGTIIGHELTHGYDDWGGQYDRSGNLLHWTEASYS

620 630 640 650 660 670
 NEP-HUM NFKEQSQCVMYQYGNFSWDLAGGQHLNGINTLGENIADNGGLGQAYRAYQNYIKKNGEEK
 * * * * * * * * * *
 NL1-MOU HFQQSQQCMYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLADGGKDQ
 ** * * * * * * * * *
 NL2-HUM HFREQSECMYQYGNYSWDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWMAEGGKDQ
 * * * * * * * * * *
 NL3-HUM RFLRKAECIVRLYDNFT...VYNQRVNGKHTLGENIADMGGLKLAYHAYQKWVREHGPEH

680 690 700 710 720 730
 NEP-HUM LLPGLDLNHHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSPGNFRIIGTLQNSAEFSEAF
 ***** * * * * * * * * *
 NL1-MOU RLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAF
 ***** * * * * * * * * *
 NL2-HUM QLPGLDLTHEQLFFINYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTF
 ** * * * * * * * * *
 NL3-HUM PLPRLKYTHDQLFFIAFAQNWCIKRRSQSIYLQVLTDKHAPEHYRVLGVSQSQFEEFGRVL

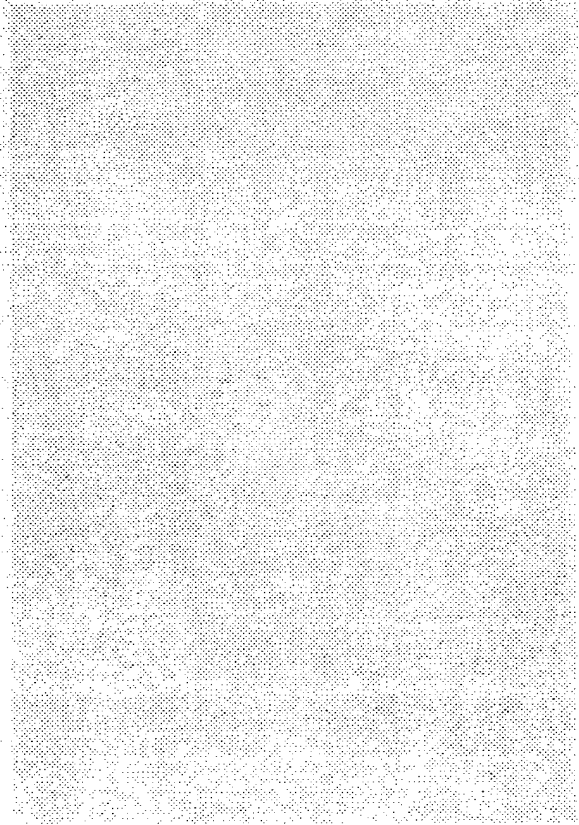
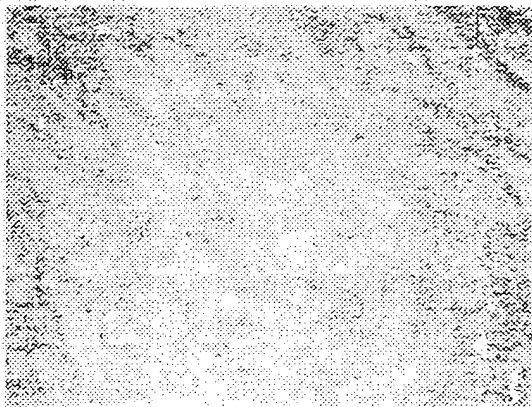
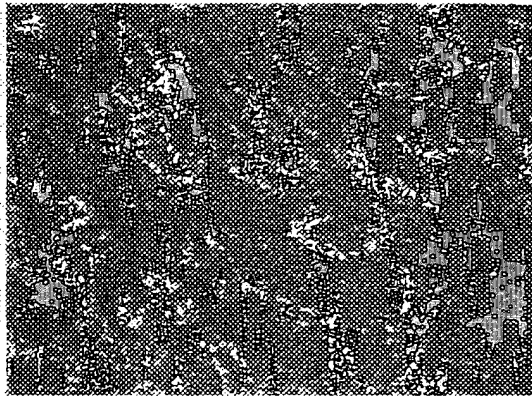
740 750
 NEP-HUM HCRKNSYMNPEKKCRVW
 ** * * * * *
 NL1-MOU HCPRGSPMHPMKRCRIW
 ** * * * * *
 NL2-HUM HCARGTPMHPKERCRVW
 ** * * * * *
 NL3-HUM HCPKVS PMNPAHKCSVW

FIG - 6 (cont'd)

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NL1 in the TESTIS



FOT290" 622ET660

FIG. 7

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Expression of PEX and NL-3 in normal and Hyp mouse embryos

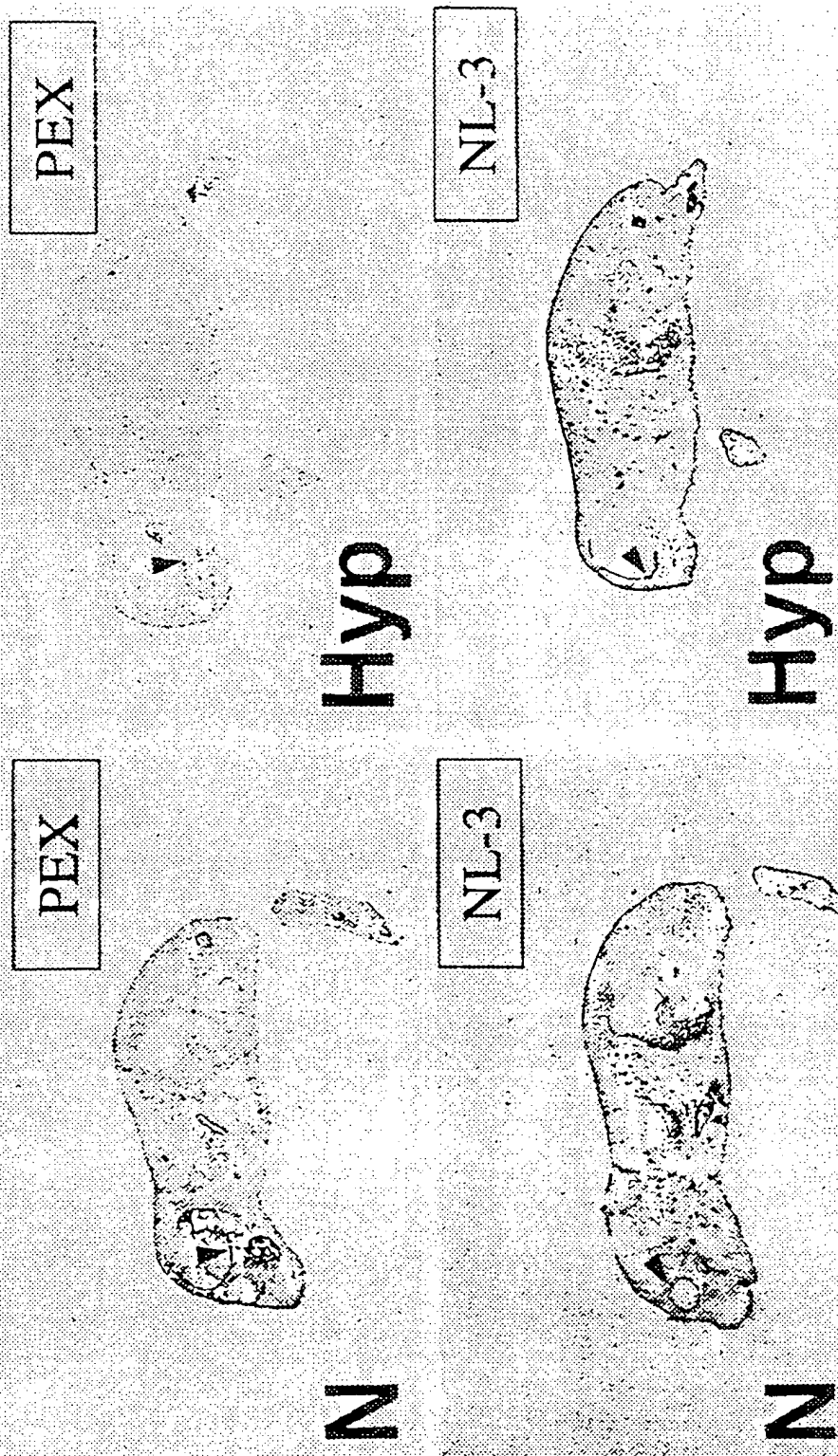
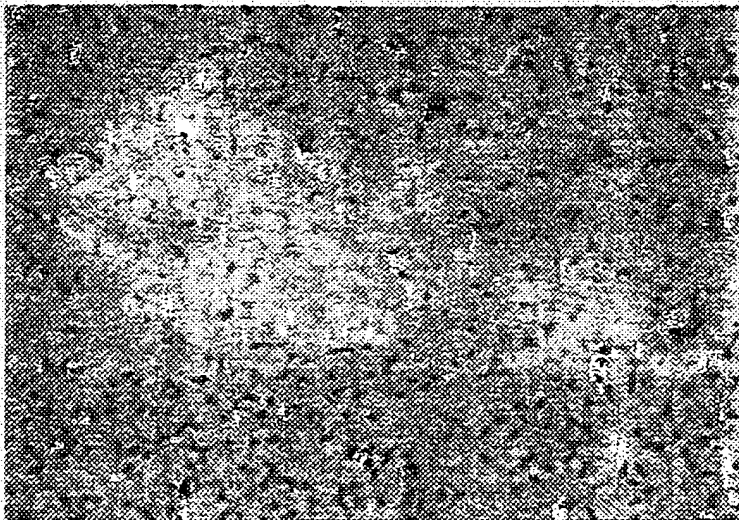
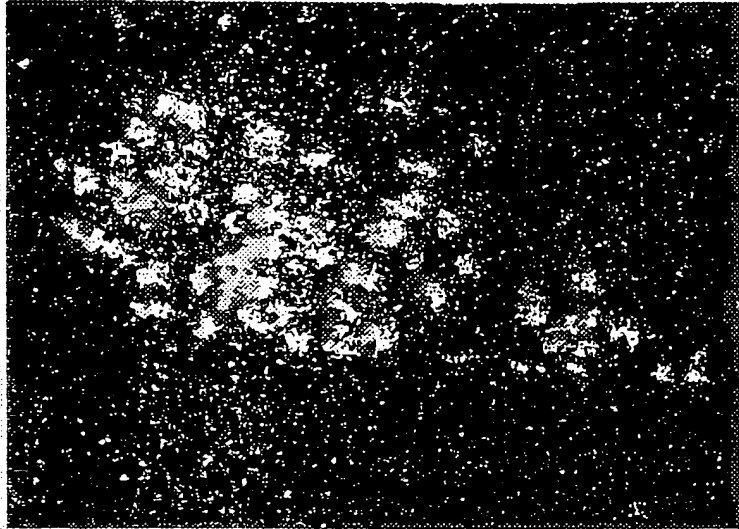


FIG. 8

FOF280 62EEF650

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NL3 in the BRAIN



FOI280" 62EEF660

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Structure and expression of NL-1

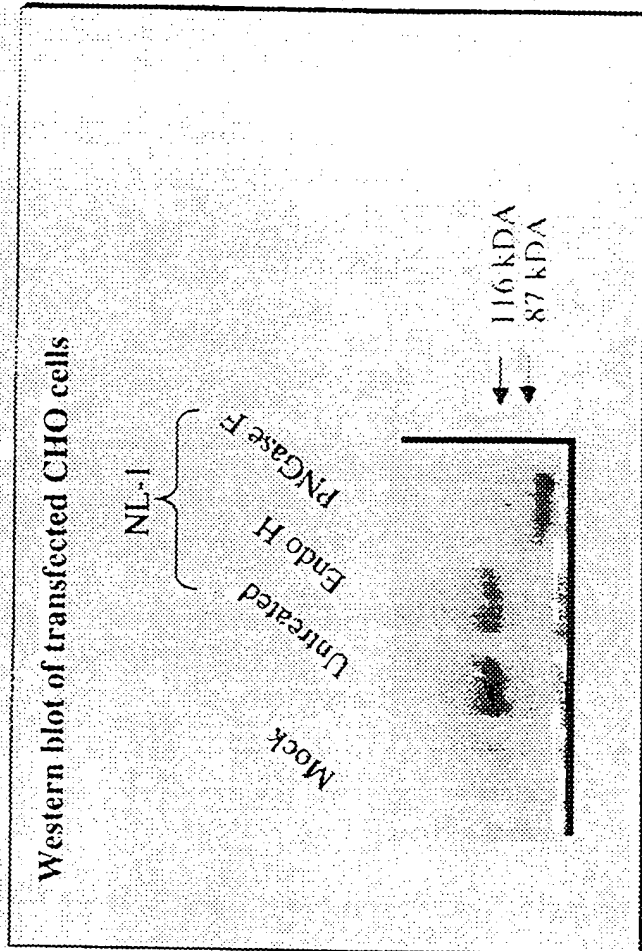
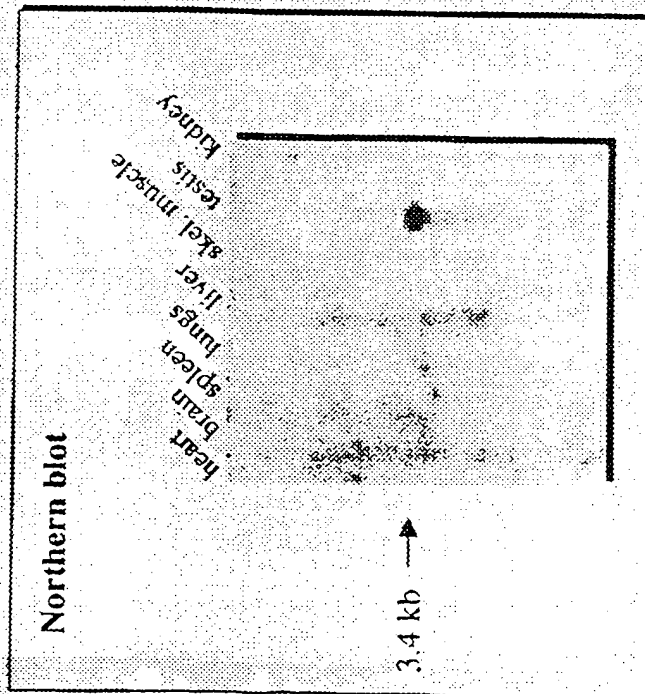
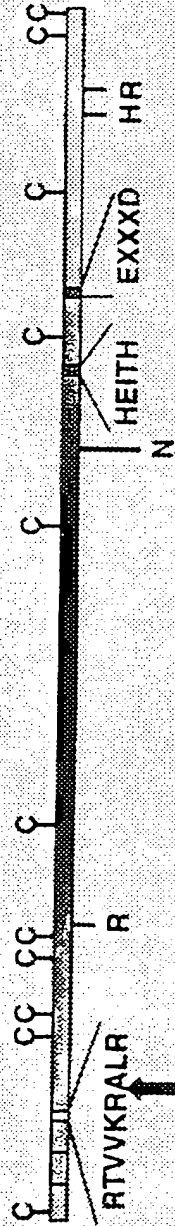
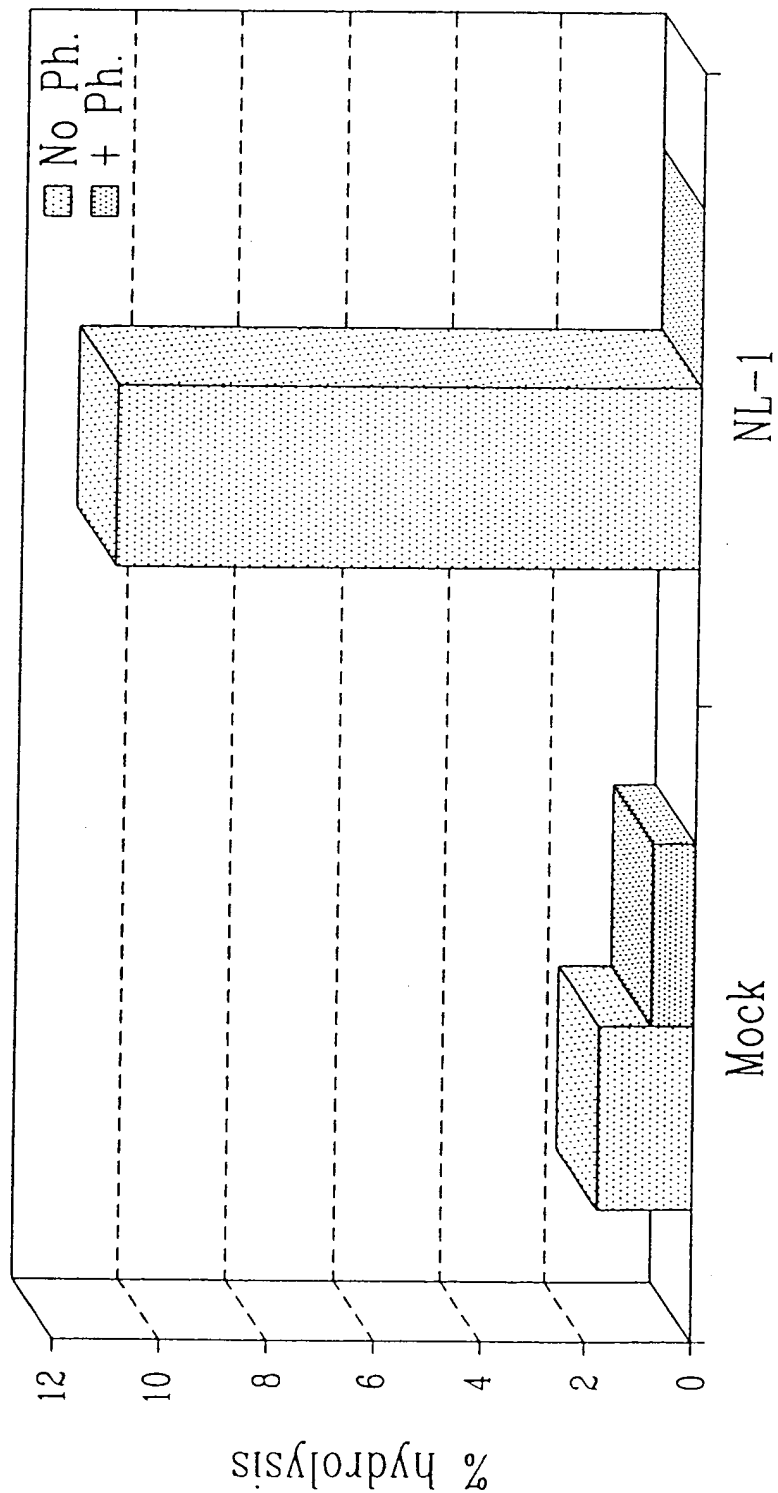


FIGURE 10

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Enzymatic activity of NL-1



Degradation of [³H]Tyr, D-Ala₂, Leu₅-enkephalin

FIG - 11

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MOCK

NL-3

CTL NL-3

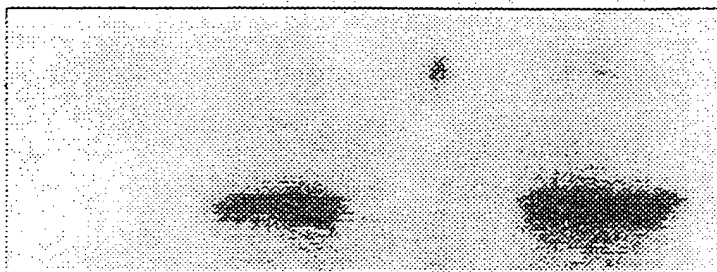


FIG. 12

FIG. 12